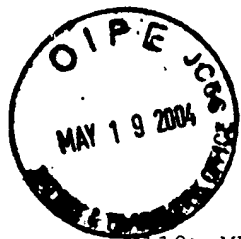


IN THE SEQUENCE LISTING

Please **replace** the Sequence Listing of record with the Substitute Sequence Listing attached hereto.



SEQUENCE LISTING

<110> MENE-SAFFRANE, Laurent
ESQUERRE-TUGAYE, Marie-Thérèse
FOURNIER, Joëlle
BEFFA, Roland
GROSJEAN-COURNOYER Marie-Claire

<120> LIPOXYGENASE OVEREXPRESSION IN PLANTS
AND REDUCTION IN PLANT SENSITIVITY TO
DISEASES AND TO ATTACKS FROM PATHOGENIC
ORGANISMS

<130> A36097-PCT-USA-A 075188.0117

<140> US/10/731,642

<141> 2003-12-08

<150> PCT/FR02/01943

<151> 2002-06-06

<150> FR 01/07470

<151> 2001-06-07

<150> FR 01/14358

<151> 2001-11-07

<160> 6

<170> Custom

<210> 1

<211> 862

<212> PRT

<213> Nicotiana tabacum

<300>

<308> X84040

<309> 1995-07-16

<400> 1

Met Phe Leu Glu Lys Ile Val Asp Ala Ile Thr Gly Lys Asp Asp Gly
1 5 10 15

Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu Asp
20 25 30

Phe Thr Asp Ile Asn Ala Ser Val Leu Asp Gly Val Leu Glu Phe Leu
35 40 45

Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp Pro
50 55 60

Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu Asn
65 70 75 80

Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe Arg

85										90					95				
Val	Thr	Phe	Asp	Trp	Asp	Asp	Glu	Glu	Phe	Gly	Val	Pro	Gly	Ala	Phe				
			100					105					110						
Ile	Ile	Lys	Asn	Leu	His	Phe	Ser	Glu	Phe	Phe	Leu	Lys	Ser	Leu	Thr				
		115					120					125							
Leu	Glu	Asp	Val	Pro	Asn	His	Gly	Lys	Val	His	Phe	Val	Cys	Asn	Ser				
	130					135					140								
Trp	Val	Tyr	Pro	Ala	Asn	Lys	Tyr	Lys	Ser	Asp	Arg	Ile	Phe	Phe	Ala				
145					150					155					160				
Asn	Gln	Ala	Tyr	Leu	Pro	Ser	Glu	Thr	Pro	Asp	Thr	Leu	Arg	Lys	Tyr				
				165					170					175					
Arg	Glu	Asn	Glu	Leu	Val	Thr	Leu	Arg	Gly	Asp	Gly	Thr	Gly	Lys	Leu				
			180					185					190						
Glu	Glu	Trp	Asp	Arg	Val	Tyr	Asp	Tyr	Ala	Tyr	Tyr	Asn	Asp	Leu	Gly				
		195					200					205							
Asp	Pro	Asp	Lys	Gly	Gln	Asp	Leu	Ser	Arg	Pro	Val	Leu	Gly	Gly	Ser				
	210					215					220								
Ser	Glu	Tyr	Pro	Tyr	Pro	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Lys	Pro	Thr				
225					230					235					240				
Lys	Thr	Asp	Pro	Asn	Ser	Glu	Ser	Arg	Ile	Pro	Leu	Leu	Met	Ser	Leu				
				245					250					255					
Asp	Ile	Tyr	Val	Pro	Arg	Asp	Glu	Arg	Phe	Gly	His	Ile	Lys	Leu	Ser				
			260					265					270						
Asp	Phe	Leu	Thr	Phe	Ala	Leu	Lys	Ser	Ile	Val	Gln	Leu	Leu	Leu	Pro				
		275					280					285							
Glu	Phe	Lys	Ala	Leu	Phe	Asp	Ser	Thr	His	Asn	Glu	Phe	Asp	Ser	Phe				
	290					295					300								
Glu	Asp	Val	Leu	Lys	Leu	Tyr	Glu	Gly	Gly	Ile	Lys	Leu	Pro	Gln	Gly				
305					310					315					320				
Pro	Leu	Leu	Lys	Ala	Ile	Thr	Asp	Ser	Ile	Pro	Leu	Glu	Ile	Leu	Lys				
			325						330					335					
Glu	Leu	Leu	Arg	Ser	Asp	Gly	Glu	Gly	Leu	Phe	Lys	Tyr	Pro	Thr	Pro				
			340					345					350						
Gln	Val	Ile	Gln	Glu	Asp	Lys	Thr	Ala	Trp	Arg	Thr	Asp	Glu	Glu	Phe				
			355				360					365							
Gly	Arg	Glu	Met	Leu	Ala	Gly	Val	Asn	Pro	Val	Ile	Ile	Ser	Arg	Leu				
	370					375					380								
Gln	Glu	Phe	Pro	Pro	Lys	Ser	Lys	Leu	Asp	Pro	Lys	Ile	Tyr	Gly	Asn				

385		390		395		400
Gln Asn Ser Thr Ile Thr Arg Glu Gln Ile Glu Asp Lys Leu Asp Gly						
	405			410		415
Leu Thr Ile Asp Glu Ala Ile Lys Thr Asn Arg Leu Phe Ile Leu Asn						
	420			425		430
His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser Thr						
	435			440		445
Asp Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp Asn						
	450			455		460
Gly Thr Leu Lys Pro Ser Ala Ile Glu Leu Ser Leu Pro His Pro Asp						
465		470		475		480
Gly Asp Gln Phe Gly Ala Val Ser Lys Val Tyr Thr Pro Ala Asp Gln						
	485			490		495
Gly Val Glu Gly Ser Ile Trp Gln Leu Ala Lys Ala Tyr Ala Ala Val						
	500			505		510
Asn Asp Ser Gly Val His Gln Leu Ile Ser His Trp Leu Asn Thr His						
	515			520		525
Ala Ala Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Ala						
	530			535		540
Leu His Pro Ile Tyr Lys Leu Leu His Pro His Phe Arg Glu Thr Met						
545		550		555		560
Asn Ile Asn Ala Leu Ala Arg Gln Ile Leu Ile Asn Gly Gly Gly Leu						
	565			570		575
Leu Glu Leu Thr Val Phe Pro Ala Lys Tyr Ser Met Glu Met Ser Ala						
	580			585		590
Val Val Tyr Lys Asp Trp Val Phe Pro Glu Gln Ala Leu Pro Thr Asp						
	595			600		605
Leu Ile Lys Arg Gly Val Ala Val Glu Asp Ser Ser Ser Pro Leu Gly						
	610			615		620
Ile Arg Leu Leu Ile Gln Asp Tyr Pro Tyr Ala Val Asp Gly Leu Lys						
625		630		635		640
Ile Trp Ser Ala Ile Lys Ser Trp Val Thr Glu Tyr Cys Asn Tyr Tyr						
	645			650		655
Tyr Lys Ser Asp Asp Ala Val Gln Lys Asp Thr Glu Leu Gln Ala Trp						
	660			665		670
Trp Lys Glu Leu Arg Glu Glu Gly His Gly Asp Lys Lys Asp Glu Pro						
	675			680		685
Trp Trp Pro Lys Met Gln Thr Val Gln Glu Leu Ile Asp Ser Cys Thr						

690	695	700
Ile Thr Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly 705 710 715 720		
Gln Tyr Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Leu Ser Arg 725 730 735		
Asn Phe Met Pro Glu Pro Gly Ser Pro Glu Tyr Glu Glu Leu Lys Thr 740 745 750		
Asn Pro Asp Lys Val Phe Leu Lys Thr Ile Thr Pro Gln Leu Gln Thr 755 760 765		
Leu Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Arg His Ser Ser Asp 770 775 780		
Thr Leu Tyr Leu Gly Gln Arg Glu Ser Pro Glu Trp Thr Lys Asp Gln 785 790 795 800		
Glu Pro Leu Ser Ala Phe Ala Arg Phe Gly Lys Lys Leu Ser Asp Ile 805 810 815		
Glu Asp Gln Ile Met Gln Met Asn Val Asp Glu Lys Trp Lys Asn Arg 820 825 830		
Ser Gly Pro Val Lys Val Pro Tyr Thr Leu Leu Phe Pro Thr Ser Glu 835 840 845		
Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile 850 855 860		

<210> 2
 <211> 3390
 <212> DNA
 <213> Artificial sequence

<220>
 <223> construct CaMV 35S-LOX

<220>
 <221> promoter
 <222> (1)..(532)
 <223> CaMV 35S promoter

<220>
 <221> CDS
 <222> (543)..(3131)
 <223> Tobacco LOX1 coding sequence

<220>
 <221> terminator
 <222> (3138)..(3390)
 <223> Nos terminator

<400> 2

```

ccatggagtc aaagattcaa atagaggacc taacagaact cgccgtaaag actggcgaac 60
agttcataca gagtctctta cgactcaatg acaagaagaa aatcttcgtc aacatgggtgg 120
agcacgacac gcttgtctac tccaaaaata tcaaagatac agtctcagaa gaccaaaggg 180
caattgagac ttttcaacaa agggtaatat ccggaaacct cctcggattc cattgcccag 240
ctatctgtca ctttattgtg aagatagtgg aaaaggaagg tggctcctac aaatgccatc 300
attgcgataa aggaaaggcc atcgttgaag atgcctctgc cgacagtggc cccaaagatg 360
gacccccacc cacgaggagc atcgtggaaa aagaagacct tccaaccacg tcttcaaagc 420
aagtggattg atgtgatatc tccactgacg taagggatga cgcacaatcc cactatcctt 480
cgcaagaccc ttcctcctat aaggaagttc atttcatttg gagaggacac gcggtaccca 540

aa atg ttt ctg gag aag att gtg gat gca atc aca ggg aaa gat gat 587
Met Phe Leu Glu Lys Ile Val Asp Ala Ile Thr Gly Lys Asp Asp
1 5 10 15

gga aaa aag gta aaa gga aca gtg gtt ttg atg aag aaa aat gtt ttg 635
Gly Lys Lys Val Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu
20 25 30

gat ttt act gat att aat gcc tca gtt ctt gat gga gtt ctt gag ttc 683
Asp Phe Thr Asp Ile Asn Ala Ser Val Leu Asp Gly Val Leu Glu Phe
35 40 45

ctt ggt cgg agg gtc tct ctc gag ttg atc agt tct gtt aat gct gat 731
Leu Gly Arg Arg Val Ser Leu Glu Leu Ile Ser Ser Val Asn Ala Asp
50 55 60

cct gca aat ggt tta caa ggg aaa cgc agc aaa gca gca tat ttg gag 779
Pro Ala Asn Gly Leu Gln Gly Lys Arg Ser Lys Ala Ala Tyr Leu Glu
65 70 75

aac tgg cta aca aat agc acc cca ata gca gca ggt gaa tca gca ttt 827
Asn Trp Leu Thr Asn Ser Thr Pro Ile Ala Ala Gly Glu Ser Ala Phe
80 85 90 95

aga gtc aca ttt gat tgg gat gat gag gaa ttt gga gtt cca gga gca 875
Arg Val Thr Phe Asp Trp Asp Asp Glu Glu Phe Gly Val Pro Gly Ala
100 105 110

ttc att atc aag aac ttg cat ttt agt gag ttc ttc ctc aag tca ctc 923
Phe Ile Ile Lys Asn Leu His Phe Ser Glu Phe Phe Leu Lys Ser Leu
115 120 125

acc ctt gaa gat gtt cct aat cat ggc aaa gtt cat ttt gtc tgt aat 971
Thr Leu Glu Asp Val Pro Asn His Gly Lys Val His Phe Val Cys Asn
130 135 140

tct tgg gtt tat cct gct aat aaa tat aag tca gat cgc atc ttc ttc 1019
Ser Trp Val Tyr Pro Ala Asn Lys Tyr Lys Ser Asp Arg Ile Phe Phe
145 150 155

```

gcg aat cag gct tat cta cca agt gaa aca cca gac aca ttg cga aaa	1067
Ala Asn Gln Ala Tyr Leu Pro Ser Glu Thr Pro Asp Thr Leu Arg Lys	
160 165 170 175	
tac aga gaa aat gaa tta gta acc tta aga gga gat gga act gga aag	1115
Tyr Arg Glu Asn Glu Leu Val Thr Leu Arg Gly Asp Gly Thr Gly Lys	
180 185 190	
ctt gag gaa tgg gat aga gtt tat gac tat gct tac tac aat gac ttg	1163
Leu Glu Glu Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu	
195 200 205	
ggt gat cca gac aaa ggc caa gat ttg tca agg cct gtc tta gga gga	1211
Gly Asp Pro Asp Lys Gly Gln Asp Leu Ser Arg Pro Val Leu Gly Gly	
210 215 220	
tct tct gag tac ccg tat cct cgt aga ggc agg aca ggc cgc aaa cca	1259
Ser Ser Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Lys Pro	
225 230 235	
acc aaa aca gat cct aat tcc gag agc agg att cca ttg ctt atg agc	1307
Thr Lys Thr Asp Pro Asn Ser Glu Ser Arg Ile Pro Leu Leu Met Ser	
240 245 250 255	
tta gac ata tat gtg cca agg gac gag cga ttt ggt cat ata aag ttg	1355
Leu Asp Ile Tyr Val Pro Arg Asp Glu Arg Phe Gly His Ile Lys Leu	
260 265 270	
tca gac ttc ttg aca ttt gct ttg aaa tcc att gtg cag ttg ctt ctc	1403
Ser Asp Phe Leu Thr Phe Ala Leu Lys Ser Ile Val Gln Leu Leu Leu	
275 280 285	
cct gag ttt aag gct ttg ttc gat agc acg cat aat gag ttt gat agt	1451
Pro Glu Phe Lys Ala Leu Phe Asp Ser Thr His Asn Glu Phe Asp Ser	
290 295 300	
ttt gag gat gta ctt aaa ctg tat gaa gga gga atc aag ttg cct caa	1499
Phe Glu Asp Val Leu Lys Leu Tyr Glu Gly Gly Ile Lys Leu Pro Gln	
305 310 315	
ggc cct ttg ttg aaa gcc att act gat agc att cct tta gag ata cta	1547
Gly Pro Leu Leu Lys Ala Ile Thr Asp Ser Ile Pro Leu Glu Ile Leu	
320 325 330 335	
aaa gaa ctc ctt cga agt gat ggt gaa ggc cta ttt aag tac cca act	1595
Lys Glu Leu Leu Arg Ser Asp Gly Glu Gly Leu Phe Lys Tyr Pro Thr	
340 345 350	
cct cag gtt att caa gag gat aaa act gca tgg agg acg gat gaa gaa	1643
Pro Gln Val Ile Gln Glu Asp Lys Thr Ala Trp Arg Thr Asp Glu Glu	
355 360 365	
ttt ggg aga gaa atg ttg gcg gga gtc aat cct gtc ata atc agt aga	1691
Phe Gly Arg Glu Met Leu Ala Gly Val Asn Pro Val Ile Ile Ser Arg	
370 375 380	

ctc	caa	gaa	ttc	cct	ccg	aaa	agc	aag	ttg	gat	cct	aaa	ata	tat	ggc	1739
Leu	Gln	Glu	Phe	Pro	Pro	Lys	Ser	Lys	Leu	Asp	Pro	Lys	Ile	Tyr	Gly	
	385					390					395					
aac	caa	aac	agt	aca	att	acc	aga	gag	cag	ata	gag	gat	aag	ttg	gat	1787
Asn	Gln	Asn	Ser	Thr	Ile	Thr	Arg	Glu	Gln	Ile	Glu	Asp	Lys	Leu	Asp	
400					405					410					415	
gga	cta	aca	att	gat	gag	gca	atc	aag	act	aac	aga	cta	ttc	ata	ttg	1835
Gly	Leu	Thr	Ile	Asp	Glu	Ala	Ile	Lys	Thr	Asn	Arg	Leu	Phe	Ile	Leu	
				420					425					430		
aac	cat	cat	gat	atc	ctt	atg	cca	tac	ttg	agg	aga	att	aac	acg	tcg	1883
Asn	His	His	Asp	Ile	Leu	Met	Pro	Tyr	Leu	Arg	Arg	Ile	Asn	Thr	Ser	
			435					440					445			
aca	gac	aca	aaa	acc	tat	gcc	tca	aga	act	ctg	ctc	ttc	ttg	caa	gat	1931
Thr	Asp	Thr	Lys	Thr	Tyr	Ala	Ser	Arg	Thr	Leu	Leu	Phe	Leu	Gln	Asp	
	450						455					460				
aat	gga	act	ttg	aag	cca	tca	gca	att	gaa	cta	agc	ttg	cca	cat	cca	1979
Asn	Gly	Thr	Leu	Lys	Pro	Ser	Ala	Ile	Glu	Leu	Ser	Leu	Pro	His	Pro	
	465					470					475					
gac	gga	gat	caa	ttt	ggc	gct	gtt	agc	aaa	gta	tat	aca	cca	gct	gat	2027
Asp	Gly	Asp	Gln	Phe	Gly	Ala	Val	Ser	Lys	Val	Tyr	Thr	Pro	Ala	Asp	
480					485					490					495	
caa	ggt	gtt	gaa	ggt	tct	atc	tgg	cag	ttg	gcc	aaa	gcc	tat	gca	gca	2075
Gln	Gly	Val	Glu	Gly	Ser	Ile	Trp	Gln	Leu	Ala	Lys	Ala	Tyr	Ala	Ala	
				500						505				510		
gtg	aat	gat	tcg	ggc	gtt	cat	caa	ctc	atc	agt	cac	tgg	ttg	aat	aca	2123
Val	Asn	Asp	Ser	Gly	Val	His	Gln	Leu	Ile	Ser	His	Trp	Leu	Asn	Thr	
			515					520					525			
cat	gca	gcg	ata	gag	cca	ttc	gtg	atc	gca	aca	aat	agg	caa	cta	agc	2171
His	Ala	Ala	Ile	Glu	Pro	Phe	Val	Ile	Ala	Thr	Asn	Arg	Gln	Leu	Ser	
		530					535					540				
gcg	ctt	cac	cct	att	tat	aag	ctt	ctc	cac	cct	cat	ttc	cgt	gag	acg	2219
Ala	Leu	His	Pro	Ile	Tyr	Lys	Leu	Leu	His	Pro	His	Phe	Arg	Glu	Thr	
	545					550					555					
atg	aac	ata	aat	gct	tta	gca	aga	cag	atc	ttg	atc	aac	ggt	ggt	gga	2267
Met	Asn	Ile	Asn	Ala	Leu	Ala	Arg	Gln	Ile	Leu	Ile	Asn	Gly	Gly	Gly	
560					565					570					575	
ctt	ctt	gag	ttg	aca	gtt	ttt	ccg	gcc	aaa	tat	tcc	atg	gaa	atg	tca	2315
Leu	Leu	Glu	Leu	Thr	Val	Phe	Pro	Ala	Lys	Tyr	Ser	Met	Glu	Met	Ser	
				580					585					590		
gca	gta	gtt	tac	aaa	gac	tgg	gtt	ttc	cct	gaa	caa	gca	ctt	cct	act	2363
Ala	Val	Val	Tyr	Lys	Asp	Trp	Val	Phe	Pro	Glu	Gln	Ala	Leu	Pro	Thr	
			595					600					605			
gat	ctc	atc	aaa	aga	gga	gta	gct	gtt	gag	gac	tcg	agc	tcc	cca	ctt	2411

Asp	Leu	Ile	Lys	Arg	Gly	Val	Ala	Val	Glu	Asp	Ser	Ser	Ser	Pro	Leu		
	610						615					620					
ggc	att	cga	tta	ctg	att	cag	gac	tat	cca	tat	gct	gtt	gat	ggg	ttg	2459	
Gly	Ile	Arg	Leu	Leu	Ile	Gln	Asp	Tyr	Pro	Tyr	Ala	Val	Asp	Gly	Leu		
	625					630					635						
aaa	att	tgg	tca	gca	att	aaa	agt	tgg	gta	act	gaa	tac	tgc	aac	tac	2507	
Lys	Ile	Trp	Ser	Ala	Ile	Lys	Ser	Trp	Val	Thr	Glu	Tyr	Cys	Asn	Tyr		
	640					645				650					655		
tat	tac	aaa	tca	gat	gat	gcg	gtt	caa	aaa	gac	act	gaa	ctc	caa	gcc	2555	
Tyr	Tyr	Lys	Ser	Asp	Asp	Ala	Val	Gln	Lys	Asp	Thr	Glu	Leu	Gln	Ala		
				660				665						670			
tgg	tgg	aag	gaa	ctc	cgc	gaa	gag	gga	cac	ggt	gac	aag	aaa	gat	gag	2603	
Trp	Trp	Lys	Glu	Leu	Arg	Glu	Glu	Gly	His	Gly	Asp	Lys	Lys	Asp	Glu		
			675					680					685				
cct	tgg	tgg	cct	aaa	atg	cag	aca	gtg	caa	gaa	ttg	ata	gac	tct	tgc	2651	
Pro	Trp	Trp	Pro	Lys	Met	Gln	Thr	Val	Gln	Glu	Leu	Ile	Asp	Ser	Cys		
			690					695				700					
acc	atc	aca	ata	tgg	ata	gct	tca	gca	ctt	cat	gca	gca	gtc	aat	ttc	2699	
Thr	Ile	Thr	Ile	Trp	Ile	Ala	Ser	Ala	Leu	His	Ala	Ala	Val	Asn	Phe		
	705					710					715						
ggg	caa	tac	cct	tat	gct	ggt	tat	ctc	cct	aat	cgc	cct	aca	tta	agc	2747	
Gly	Gln	Tyr	Pro	Tyr	Ala	Gly	Tyr	Leu	Pro	Asn	Arg	Pro	Thr	Leu	Ser		
	720				725					730					735		
cga	aat	ttc	atg	cca	gag	cca	gga	agt	cct	gag	tat	gaa	gag	ctc	aag	2795	
Arg	Asn	Phe	Met	Pro	Glu	Pro	Gly	Ser	Pro	Glu	Tyr	Glu	Glu	Leu	Lys		
				740					745					750			
aca	aat	ccg	gat	aag	gta	ttc	ctc	aaa	aca	atc	act	cct	cag	ctg	cag	2843	
Thr	Asn	Pro	Asp	Lys	Val	Phe	Leu	Lys	Thr	Ile	Thr	Pro	Gln	Leu	Gln		
			755					760					765				
aca	ctg	ctt	ggc	att	tcc	ctc	ata	gag	atc	ttg	tca	agg	cat	tct	tcg	2891	
Thr	Leu	Leu	Gly	Ile	Ser	Leu	Ile	Glu	Ile	Leu	Ser	Arg	His	Ser	Ser		
		770					775					780					
gat	aca	ctt	tac	ctc	ggg	caa	agg	gaa	tca	cct	gaa	tgg	aca	aag	gat	2939	
Asp	Thr	Leu	Tyr	Leu	Gly	Gln	Arg	Glu	Ser	Pro	Glu	Trp	Thr	Lys	Asp		
	785					790					795						
caa	gaa	cca	ctt	tca	gct	ttt	gcg	agg	ttt	gga	aag	aag	ctg	agt	gat	2987	
Gln	Glu	Pro	Leu	Ser	Ala	Phe	Ala	Arg	Phe	Gly	Lys	Lys	Leu	Ser	Asp		
	800				805					810					815		
atc	gag	gat	cag	att	atg	cag	atg	aat	gtc	gat	gag	aaa	tgg	aag	aac	3035	
Ile	Glu	Asp	Gln	Ile	Met	Gln	Met	Asn	Val	Asp	Glu	Lys	Trp	Lys	Asn		
				820					825					830			
agg	tcg	ggt	cct	gtt	aaa	gtt	cca	tac	acc	ttg	ctc	ttc	ccc	aca	agt	3083	
Arg	Ser	Gly	Pro	Val	Lys	Val	Pro	Tyr	Thr	Leu	Leu	Phe	Pro	Thr	Ser		

835

840

845

gaa gga gga ctt act ggc aaa gga att cct aac agt gtg tca ata tag 3131
Glu Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile
850 855 860

aactttcccg atctagtaac atagatgaca ccgcgcgcga taatttatcc tagtttgccg 3191
gctatatattt gttttctatc gcgtattaaa tgtataattg cgggactcta atcataaaaa 3251
cccatctcat aaataacgtc atgcattaca tgттаattat tacatgctta acgtaattca 3311
acagaaatta tatgataatc atcgcaagac cggcaacagg attcaatctt aagaaacttt 3371
attgccaaat gtttgaacg 3390

<210> 3
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: Sense
primer

<400> 3
gttatcaaac agtttaaaat gtttctggag 30

<210> 4
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: Reverse
primer

<400> 4
tgatttaaag ttctatattg ac 22

<210> 5
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: Primer F

<400> 5
ggccatggag tcaaagattc 20

<210> 6
<211> 19

<212> DNA
<213> Artificial sequence

<220>
<223> Artificial sequence description: Primer R

<400> 6
gctctggcat gaaatttcg